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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Jun 08 19:36:04 EDT 2007

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Application No: 10661742 Version No: 1.1

Input Set:

Output Set:

Started: 2007-06-08 19:35:50.118
Finished: 2007-06-08 19:35:56.264
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 146 ms
Total Warnings: 15
Total Errors: 26
No. of SeqIDs Defined: 19
Actual SeqID Count: 19

Input Set:

Output Set:

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Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 146 ms
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No. of SeqIDs Defined: 19
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Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (17)
E 257	Invalid sequence data feature in <221> in SEQ ID (17)
E 257	Invalid sequence data feature in <221> in SEQ ID (17)
E 257	Invalid sequence data feature in <221> in SEQ ID (17)
E 257	Invalid sequence data feature in <221> in SEQ ID (17)
E 257	Invalid sequence data feature in <221> in SEQ ID (17)
E 257	Invalid sequence data feature in <221> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
E 257	Invalid sequence data feature in <221> in SEQ ID (19)
E 257	Invalid sequence data feature in <221> in SEQ ID (19)
E 257	Invalid sequence data feature in <221> in SEQ ID (19)
E 257	Invalid sequence data feature in <221> in SEQ ID (19)
E 257	Invalid sequence data feature in <221> in SEQ ID (19)
E 257	Invalid sequence data feature in <221> in SEQ ID (19)
E 257	Invalid sequence data feature in <221> in SEQ ID (19)
E 257	Invalid sequence data feature in <221> in SEQ ID (19) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> ROJER, EVA

<120> REARRANGED SQUAMOUS CELL CARCINOMA ANTIGEN GENES II

<130> 7274

<140> 10/661,742

<141> 2003-09-12

<150> PCT/SE02/00512

<151> 2002-03-15

<150> SE 0100938

<151> 2001-03-15

<160> 19

<170> PatentIn Ver. 3.3

<210> 1

<211> 390

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<400> 1

Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
1 5 10 15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
20 25 30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
35 40 45

Thr Ala Gln Gln Ile Lys Lys Val Leu His Phe Asp Gln Val Thr Glu
50 55 60

Asn Thr Thr Gly Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
85 90 95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
100 105 110

Tyr Leu Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
115 120 125

Thr Ser Val Glu Ser Val Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
130 135 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145 150 155 160

Asn Leu Ile Pro Glu Gly Asn Ile Gly Ser Asn Thr Thr Leu Val Leu
165 170 175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
180 185 190

Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
195 200 205

Ser Ile Gln Met Met Arg Gln Tyr Thr Ser Phe His Phe Ala Ser Leu
210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225 230 235 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
245 250 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
260 265 270

Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
275 280 285

Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
290 295 300

Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
305 310 315 320

His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
325 330 335

Thr Glu Glu Gly Val Glu Ala Ala Ala Ala Thr Ala Val Val Val
340 345 350

Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
355 360 365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
370 375 380

Gly Arg Phe Ser Ser Pro
385 390

<210> 2

<211> 1193

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

construct

<400> 2

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gtcctcttag gagccaaaga caacactgca caacagatta agaaggttct tcactttatg 180
caagtcacag agaacaccac agaaaaagct gcaacatatac atgttgatag gtcagggaaat 240
gttcatcacc agtttcaaaa gcttctgact gaattcaaca aattccactg atgcatatga 300
gctgaagatc gccaacaagc tcttcggaga aaaaacgtat ctatTTTAC aggaatattt 360
agatgccatc aagaattttt accagaccag tgtggaatct gttgattttg caaatgtcc 420
agaagaaagt cgaaaagaaga ttaactcctg ggtggaaagt caaacgaatg aaaaaattaa 480
aaacctaatt cctgaaggta atattggcag caataccaca ttggttcttg tgaacgcaat 540
ctatTTCAAA gggcagtggg agaagaaatt taataaagaa gatactaaag aggaaaaattt 600
ttggccaaac aagaatacat acaaagtccat acagatgtg aggcaataca catTTTCA 660
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tctaaggatg attgtgttgc tgccaaatga aatcgatggt ctccagaagc ttgaagagaa 780
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cgatttacac ttacctcggt tcaaaatggaa agagagctat gacctaagg acacgtttag 900
aaccatggga atggtaata tcttcaatgg ggatgcagac ctctcaggca tgacctggag 960
ccacggtctc tcagtatcta aagtcttaca caaggccttt gtggaggtca ctgaggaggg 1020
agtggaaagct gcagctgcca ccgctgttagt agtagtcgaa ttatcatctc cttcaactaa 1080
tgaagagttc tggtaatc accctttccattttccata aggcaaaata agaccaacag 1140
catcctcttc tatggcagat tctcatcccc atagatgcaat ttagtgtgtc act 1193

<210> 3

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 3

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29

<210> 4

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 4

gagctcgagt ctcatcagtg acagactaat tgcata

38

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 5

tggaaatggac aagtttgca

20

<210> 6

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 6

gttaggactcc agatagcac

19

<210> 7

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 7

tggagccacg gtctctcag

19

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 8

attagttgaa ggagatgata attc

24

<210> 9

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 9

aatacataca agtcca

16

<210> 10
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 10
ggactttaga tactga

16

<210> 11
<211> 1170
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic construct

<400> 11
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gtcctcttag gagccaaaga caacactgca caacagatta agaaggttct tcactttgat 180
caagtccac agaacaccac agaaaaagct gcaacatatac atgttgatag gtcaggaaat 240
gttcatcacc agtttcaaaa gcttctgact gaattcaaca aatccactga tgcataatgag 300
ctgaagatcg ccaacaagct ctcggagaa aaaacgtatc tattttaca ggaatattta 360
gatgccatca agaaatttta ccagaccagt gtggaatctg ttgattttgc aaatgctcca 420
gaagaaaatgc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaatttaaa 480
aacctaattc ctgaaggtaa tattggcagc aataccacat tggttcttgtt gAACGCAATC 540
tatttcaaag ggcagtgaaa gaagaaaattt aataaagaag atactaaaga ggaaaaattt 600
tggccaaaca agaatacata caagtccata cagatgatga ggcaatacac atctttcat 660
tttgcctcgc tggaggatgt acaggccaag gtcctggaaa taccatacaa aggcaagat 720
ctaagcatga ttgtgttgct gccaaatgaa atcgatggc tccagaagct tgaagagaaa 780
ctcaactgctg agaaattgtat ggaatggaca agtttgcaga atatgagaga gacatgtgtc 840
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accatgggaa tggtaatat ctcataatgg gatgcagacc tctcaggcat gacctggagc 960
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gaagagttct gttgtatca cccttcataa ggcaaaataa gaccaacagc 1140
atcctttct atggcagatt ctcatacccc 1170

<210> 12
<211> 1173
<212> DNA
<213> Homo sapiens

<400> 12
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gtcctcttag gagccaaaga caacactgca caacagatta agaaggttct tcactttgat 180
caagtccac agaacaccac agaaaaagct gcaacatatac atgttgatag gtcaggaaat 240

gttcatcacc agttcaaaa gcttctgact gaattcaaca aatccactga tgcataatgag 300
ctgaagatcg ccaacaagct ctcggagaa aaaacgtatc tattttaca ggaatattta 360
gatgccatca agaaattta ccagaccagt gtggaatctg ttgatttgc aaatgctcca 420
gaagaaaagtc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaattaaa 480
aacctaattc ctgaaggtaa tattggcagc aataccacat tggttcttgt gaacgcaatc 540
tatttcaaag ggcagtggga gaagaaattt aataaagaag atactaaaga ggaaaaattt 600
tggccaaaca agaatacata caagtccata cagatgatga ggcaatacac atctttcat 660
tttgccctcg tggaggatgt acaggccaag gtcctggaaa taccatacaa aggcaaagat 720
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ctcaactgctg agaaattgat ggaatggaca agttgcaga atatgagaga gacacgtgtc 840
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cgccgtctcg tgctatctgg agtcctacac aaggcccttg tggaggttac agaggaggg 1020
gcagaagctg cagctgccac cgctgttagta ggattcggat catcacctac ttcaactaat 1080
gaagagttcc attgtaatca cccttccta ttcttcataa ggcaaaataa gaccaacagc 1140
atcctttct atggcagatt ctcatacccc tag 1173

<210> 13
<211> 1173
<212> DNA
<213> Homo sapiens

<400> 13
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aaatcaaaaag agaacaacat cttctattcc cctatcagca tcacatcagc attaggatg 120
gtcctcttag gagccaaaga caacactgca caacaatta gcaagggtct tcactttgtat 180
caagtcacag agaacaccac agaaaaaagct gcaacatatc atgttgatag gtcagggaaat 240
gttcatcacc agttcaaaa gcttctgact gaattcaaca aatccactga tgcataatgag 300
ctgaagatcg ccaacaagct ctgcggagaa aagacgtatc aattttaca ggaatattta 360
gatgccatca agaaattta ccagaccagt gtggaatcta ctgatttgc aaatgctcca 420
gaagaaaagtc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaattaaa 480
aacctatttc ctgatggac tattggcaat gatacgacac tggttcttgt gaacgcaatc 540
tatttcaaag ggcagtggga gaataaattt aaaaaagaaa acactaaaga ggaaaaattt 600
tggccaaaca agaatacata caaatctgtt cagatgatga ggcaatacaa ttcccttaat 660
tttgccctgc tggaggatgt acaggccaag gtcctggaaa taccatacaa aggcaaagat 720
ctaagcatga ttgtgtgc gccaaatgaa atcgatggtc tgcagaagct tgaagagaaa 780
ctcaactgctg agaaattgat ggaatggaca agttgcaga atatgagaga gacatgtgtc 840
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cacggctctc cagtatctaa agtcctacac aaggcccttg tggaggtcac tgaggaggg 1020
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atcctttct atggcagatt ctcatacccc tag 1173

<210> 14
<211> 390
<212> PRT
<213> Homo sapiens

<400> 14
Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
1 5 10 15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
20 25 30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
35 40 45

Thr Ala Gln Gln Ile Lys Lys Val Leu His Phe Asp Gln Val Thr Glu
50 55 60

Asn Thr Thr Gly Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
85 90 95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
100 105 110

Tyr Leu Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
115 120 125

Thr Ser Val Glu Ser Val Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
130 135 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145 150 155 160

Asn Leu Ile Pro Glu Gly Asn Ile Gly Ser Asn Thr Thr Leu Val Leu
165 170 175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
180 185 190

Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
195 200 205

Ser Ile Gln Met Met Arg Gln Tyr Thr Ser Phe His Phe Ala Ser Leu
210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225 230 235 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
245 250 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
260 265 270

Gln Asn Met Arg Glu Thr Arg Val Asp Leu His Leu Pro Arg Phe Lys
275 280 285

Val Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
290 295 300

Val Asp Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Gly Ser
305 310 315 320

Arg Gly Leu Val Leu Ser Gly Val Leu His Lys Ala Phe Val Glu Val
325 330 335

Thr Glu Glu Gly Ala Glu Ala Ala Ala Ala Thr Ala Val Val Gly Phe
340 345 350

Gly Ser Ser Pro Ala Ser Thr Asn Glu Glu Phe His Cys Asn His Pro
355 360 365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
370 375 380

Gly Arg Phe Ser Ser Pro
385 390

<210> 15
<211> 390
<212> PRT
<213> Homo sapiens

<400> 15
Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
1 5 10 15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
20 25 30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
35 40 45

Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
50 55 60

Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
85 90 95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
100 105 110

Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
115 120 125

Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
130 135 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145 150 155 160

Asn Leu Phe Pro Asp Gly Thr Ile Gly Asn Asp Thr Thr Leu Val Leu
165 170 175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys
180 185 190

Glu Asn Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys

195

200

205

Ser Val Gln Met Met Arg Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu
210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225 230 235 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
245 250 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
260 265 270

Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys